RAW SEQUENCE LISTING

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Application Serial Number: _____ 10/559,711 _____
Source: _____ IFWP _____
Date Processed by STIC: _____ 02/10/2007 _____

ENTERED

IFWP

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 3 <110> APPLICANT: Croker, Ben
 4        Roberts, Andrew
 5        Metcalf, Don
 6        Alexander, Warren
 7        Hilton, Doug
 8        Nicola, Nicos
10 <120> TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS WHICH MODULATE
11        GRANULOCITE-COLONY STIMULATING FACTOR (G-CSF) DEPENDENT
12        PROCESSES BY MODULATION OF THE LEVELS OF SUPPRESSOR OF
13        CYTOKINE SIGNALING (SOCS)
15 <130> FILE REFERENCE: 19413
17 <140> CURRENT APPLICATION NUMBER: 10/559,711
18 <141> CURRENT FILING DATE: 2005-12-05
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 682
26 <212> TYPE: DNA
27 <213> ORGANISM: human
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(678)
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38 gac acc agc ctg cgc ctc aag acc ttc agc tcc aag agc gag tac cag      96
39 Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln
40                 20                  25                  30
42 ctg gtg gtg aac gca gtg cgc aag ctg cag gag agc ggc ttc tac tgg     144
43 Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp
44             35                  40                  45
46 agc gca gtg acc ggc ggc gag gcg aac ctg ctg ctc agc gcc gag ccc     192
47 Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro
48         50                  55                  60
50 gcc ggc acc ttt ctg atc cgc gac agc tcg gac cag cgc cac ttc ttc     240
51 Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe
52 65                  70                  75                  80
54 acg ctc agc gtc aag acc cag tct ggg acc aag aac ctg cgc atc cag     288
55 Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln
56                 85                  90                  95
58 tgt gag ggg ggc agc ttc tct ctg cag agc gat ccc cgg agc acg cag     336
59 Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln
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60              100                 105                 110
63 ccc gtg ccc cgc ttc gac tgc gtg ctc aag ctg gtg cac cac tac atg      384
64 Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
65              115                 120                 125
67 ccg ccc cct gga gcc ccc tcc ttc ccc tcg cca cct act gaa ccc tcc      432
68 Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser
69              130                 135                 140
71 tcc gag gtg ccc gag cag ccg tct gcc cag cca ctc cct ggg agt ccc      480
72 Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro
73 145                 150                 155                 160
75 ccc aga aga gcc tat tac atc tac tcc ggg ggc gag aag atc ccc ctg      528
76 Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu
77                  165                 170                 175
79 gtg ttg agc cgg ccc ctc tcc tcc aac gtg gcc act ctt cag cat ctc      576
80 Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu
81              180                 185                 190
83 tgt cgg aag acc gtc aac ggc cac ctg gac tcc tat gag aaa gtc acc      624
84 Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr
85                  195                 200                 205
87 cag ctg ccg ggg ccc att cgg gag ttc ctg gac cag tac gat gcc ccg      672
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98 <213> ORGANISM: human
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108 Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp
109              35                  40                  45
111 Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro
112      50                  55                  60
114 Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe
115 65                  70                  75                  80
117 Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln
118              85                  90                  95
120 Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln
121              100                 105                 110
123 Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
124              115                 120                 125
126 Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser
127      130                 135                 140
129 Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro
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RAW SEQUENCE LISTING   DATE: 02/10/2007
PATENT APPLICATION: US/10/559,711   TIME: 09:52:26

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Output Set: N:\CRF4\02102007\J559711.raw

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133                    165                    170                    175
135 Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu
136                    180                    185                    190
138 Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr
139              195                    200                    205
141 Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro
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147 <210> SEQ ID NO: 3
148 <211> LENGTH: 2187
149 <212> TYPE: DNA
150 <213> ORGANISM: murine
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161 atg agc cgc ccc ctg gac acc agc ctg cgc ctc aag acc ttc agc tcc        98
162 Met Ser Arg Pro Leu Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser
163              15                   20                   25
165 aaa agc gag tac cag ctg gtg gtg aac gcc gtg cgc aag ctg cag gag       146
166 Lys Ser Glu Tyr Gln Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu
167              30                   35                   40
169 agc gga ttc tac tgg agc gcc gtg acc ggc ggc gag gcg aac ctg ctg       194
170 Ser Gly Phe Tyr Trp Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu
171       45                   50                   55
173 ctc agc gcc gag ccc gcg ggc acc ttt ctt atc cgc gac agc tcg gac       242
174 Leu Ser Ala Glu Pro Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp
175 60                   65                   70                   75
177 cag cgc cac ttc ttc acg ttg agc gtc aag acc cag tcg ggg acc aag       290
178 Gln Arg His Phe Phe Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys
179              80                   85                   90
181 aac cta cgc atc cag tgt gag ggg ggc agc ttt tcg ctg cag agt gac       338
182 Asn Leu Arg Ile Gln Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp
183       95                  100                  105
185 ccc cga agc acg cag cca gtt ccc cgc ttc gac tgt gta ctc aag ctg       386
186 Pro Arg Ser Thr Gln Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu
187       110                  115                  120
189 gtg cac cac tac atg ccg cct cca ggg acc ccc tcc ttt tct ttg cca       434
190 Val His His Tyr Met Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro
191       125                  130                  135
193 ccc acg gaa ccc tcg tcc gaa gtt ccg gag cag cca cct gcc cag gca       482
194 Pro Thr Glu Pro Ser Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala
195 140                  145                  150                  155
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198 Leu Pro Gly Ser Thr Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly
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201 gag aag att ccg ctg gta ctg agc cga cct ctc tcc tcc aac gtg gcc      578
202 Glu Lys Ile Pro Leu Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala
203                 175                 180                 185
205 acc ctc cag cat ctt tgt cgg aag act gtc aac ggc cac ctg gac tcc      626
206 Thr Leu Gln His Leu Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser
207         190                 195                 200
209 tat gag aaa gtg acc cag ctg cct gga ccc att cgg gag ttc ctg gat      674
210 Tyr Glu Lys Val Thr Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp
211     205                 210                 215
213 cag tat gat gct cca ctt taaggagcaa aagggtcaga ggggggcctg            722
214 Gln Tyr Asp Ala Pro Leu
215 220                 225
217 ggtcggtcgg tcgcctctcc tccgaggcac atggcacaag cacaaaaatc cagccccaac    782
219 ggtcggtagc tcccagtgag ccaggggcag attggcttct tcctcaggcc ctccactccc    842
221 gcagagtaga gctggcagga cctggaattc gtctgagggg aggggagct gccacctgct     902
223 ttccsccctc ccccagctcc agcttctttc aagtggagcc agccggcctg gcctggtggg    962
225 acaatacctt tgacaagcgg actctcccct ccccttcctc cacacccct ctgcttccca    1022
227 agggaggtgg ggacacctcc aagtgttgaa cttagaactg caaggggaat cttcaaactt    1082
229 tcccgctgga acttgtttgc gctttgattt ggtttgatca agagcaggca cctgggggaa    1142
231 ggatggaaga gaaaagggtg tgtgaagggt ttttatgctg gccaaagaaa taaccactcc    1202
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253 catgccgctc acaggggcct cacgggaatg cagcagccat gcaattacct ggaactggtc    1862
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257 tgttggggtg gctttttttct ctctgttttg aataatgttt acaatttgcc tcaatcactt    1982
259 ttataaaaat ccacctccag cccgcccctc tccccactca ggccttcgag gctgtctgaa    2042
261 gatgcttgaa aaactcaacc aaatcccagt tcaactcaga cttttgcacat atatttatat    2102
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265 aaaaaaaaaa aaaaaaaaaa aaaaa                                          2187
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268 <211> LENGTH: 225
269 <212> TYPE: PRT
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278             20                  25                  30
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280 Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp
281         35                  40                  45
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284     50                  55                  60
286 Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe
287 65                  70                  75                  80
290 Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln
291                     85                  90                  95
293 Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln
294         100                 105                 110
296 Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val His His Tyr Met
297         115                 120                 125
299 Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro Pro Thr Glu Pro Ser
300     130                 135                 140
302 Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala Leu Pro Gly Ser Thr
303 145                 150                 155                 160
305 Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu
306                 165                 170                 175
308 Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu
309         180                 185                 190
311 Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr
312         195                 200                 205
314 Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro
315     210                 215                 220
317 Leu
318 225
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VERIFICATION SUMMARY
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